AMENDMENTS TO THE CLAIMS

1. (Previously Presented) A method for determining whether a human immunodeficiency virus type 1 ("HIV-1) has an increased likelihood of having an impaired replication capacity, comprising: detecting whether the reverse transcriptase encoded by said HIV-1 exhibits the presence or absence or a mutation associated with impaired replication capacity at amino acid positions 98, 100, 101, 106, 108, 179, 181, 188, 190, 225, 226 or 236 or the amino acid sequence of said reverse transcriptase, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having impaired replication capacity, with the proviso that said mutation is not P236L.

2. (Previously Presented) The method of claim 1, wherein the mutation associated with impaired replication capacity is selected from the group consisting of A98G, L100I, K101E, V106A, V106I, V106M, Y181C, Y188A, Y188C, Y188H, Y188L, G190A, G190C, G190E, G190T, G190V, G190Q, G190S and G190V.

3. (Original) The method of claim 1, wherein the mutation confers resistance to a non-nucleoside reverse transcriptase inhibitor.

4. (Original) The method of claim 3, wherein said reverse transcriptase inhibitor is nevirapine, delavirdine or efavirenz.

5. (Previously Presented) A method for determining whether a subject has an HIV-1 with an increased likelihood of having an impaired replication capacity, comprising: detecting whether the reverse transcriptase encoded by said HIV-1 exhibits the presence or absence of a mutation associated with impaired replication capacity at amino acid position 98, 100, 101, 106, 108, 179, 181, 188, 190, 225 or 236 of the amino acid sequence of said reverse transcriptase, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having impaired replication capacity, with the proviso that said mutation is not P236L.

6. (Previously Presented) The method of claim 5, wherein the mutation associated with impaired replication capacity is selected from the group consisting of A98G,

L100I, K101E, V106A, V106I, V106M, Y181C, Y188A, Y188C, Y188H, Y188L, G190A, G190C, G190E, G190T, G190V, G190Q, G190S and G190V.

7. (Original) The method of claim 5, wherein mutation confers resistance to a non-nucleoside reverse transcriptase inhibitor.

8. (Original) The method of claim 7, wherein said non-nucleoside reverse transcriptase inhibitor is neviripine, delavirdine or efavirenz.

9. (Original) The method of claim 5, wherein the subject is undergoing or has undergone prior treatment with an antiviral drug.

10. (Original) The method of claim 1, wherein the method comprises detecting the presence or absence or a mutation associated with impaired replication capacity at at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acid positions.

11. (Currently Amended) A method for determining whether a human immunodeficiency virus type 1 ("HIV-1") has an increased likelihood of having an impaired replication capacity, comprising detecting whether the reverse transcriptase encoded by said HIV-1 exhibits the presence or absence or a mutation associated with impaired replication capacity at amino acid positions 106 and 181; 103 and 190; [103 and 236]; 181 and 236; 103 and 188; 103 and 181; 100 and 103; or 98 and 181.

12. (Currently Amended) A method for determining whether a human immunodeficiency virus type 1 ("HIV-1" has an increased likelihood of having an impaired replication capacity, comprising detecting whether the reverse transcriptase encoded by said HIV-1 exhibits the presence or absence of a mutation associated with impaired replication capacity selected from the group consisting of: V106A and Y181C; K103N and G190S; [P236L and K103N;] P236L and Y181C; K103N and G190A; K103N and Y181C; K103N and Y188L; L100I and K103N; and Y181C and A98G.

13. (Previously Presented) The method of claim 11, wherein the method comprises detecting the presence or absence or a mutation associated with impaired

replication capacity at amino acid positions 103, 181 and 236; 100, 103 and 190; or 103, 181 and 225.

14. (Previously Presented) The method of claim 11, wherein the method comprises detecting the presence or absence or a mutation associated with impaired replication capacity selected from the group consisting of: P236L, K103N and Y181C; L100I, K103N and G190S; and K103N, Y181C and P225H.

15. (Original) The method of claim 2, wherein the method comprises detecting the presence or absence or a mutation associated with impaired replication capacity at at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acid positions.

16. (Original) The method of claim 15, wherein the method comprises detecting the presence or absence of a mutation associated with impaired replication capacity at amino acid positions 106 and 181; 103 and 190; 103 and 236; 181 and 236; 103 and 188; 103 and 181; 100 and 103; or 98 and 181.

17. (Previously Presented) The method of claim 15, wherein the method comprises detecting the presence or absence or a mutation associated with impaired replication capacity selected from the group consisting of: V106A and Y181C; K103N and G109S; K103N and G190A; K103N and Y181C; K103N and Y188L; L100I and K103N; and Y181C and A98G.

18. (Original) The method of claim 15, wherein the method comprises detecting the presence or absence of a mutation associated with impaired replication capacity at amino acid positions 103, 181 and 236; 100, 103, and 190; or 103, 181 and 225.

19. (Previously Presented) The method of claim 15, wherein the method comprises detecting the presence or absence of a mutation associated with impaired replication capacity selected from the group consisting of: L100I, K103N and G190S; and K103N, Y181C and P225H.

20. (Canceled)